

Query= SEQ ID NO:9 (PE029)
(184 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL390242.17.1.68883	<u>192</u>	5e-47
AL158844.14.1.53402	<u>78</u>	8e-13

>AL390242.17.1.68883
Length = 68883

Score = 192 bits (97), Expect = 5e-47
Identities = 97/97 (100%)
Strand = Plus / Plus

Query: 88 agcacaccaacatggcacatgtatacatatgtaacaaacctgcacattgtgcacatgtac 147
|||||
Sbjct: 3247 agcacaccaacatggcacatgtatacatatgtaacaaacctgcacattgtgcacatgtac 3306

Query: 148 cctaaaacttaaagtgtacaataataaaaattttttt 184
|||||
Sbjct: 3307 cctaaaacttaaagtgtacaataataaaaattttttt 3343

>AL158844.14.1.53402
Length = 53402

Score = 77.8 bits (39), Expect = 8e-13
Identities = 45/48 (93%)
Strand = Plus / Plus

Query: 40 actgntgtttgcaagctgnntaagtgagcaaactcttggaagatttca 87
|||||
Sbjct: 53105 actgttggtttgcaagctggttaagtgagcaaactcttggaagatttca 53152

Query= SEQ ID NO:10 (PE029)
(309 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Hom...	<u>589</u>	e-165
AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007...	<u>589</u>	e-165

>AC087564 ACCESSION:AC087564 NID: gi 28933558 gb AC087564.6 Homo sapiens
chromosome 16 clone RP11-437L7, complete sequence
Length = 157233

Score = 589 bits (297), Expect = e-165
Identities = 309/310 (99%), Gaps = 1/310 (0%)
Strand = Plus / Minus

Query: 1 ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 60
|||||
Sbjct: 105042 ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 104983

Query: 61 gtgacatggagggtccccccacctgcaagcttttggtttgctggatcttggacagtacc 120
|||||
Sbjct: 104982 gtgacatggagggtccccccacctgcaagcttttggtttgctggatcttggacagtacc 104923

Query: 121 ctggcgaaaagcattcggaagattatccggctagcacagccttcaaggaataaatatct 180
|||||
Sbjct: 104922 ctggcgaaaagcattcggaagattatccggctagcacagccttcaaggaataaatatct 104863

Query: 181 aacaccttgttccct-ttgcggttcaaaagccactgtcactgggggtacataggcagtttt 239
|||||
Sbjct: 104862 aacaccttgttcccttttgcggttcaaaagccactgtcactgggggtacataggcagtttt 104803

Query: 240 aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 299
|||||
Sbjct: 104802 aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 104743

Query: 300 gttgaaacgc 309
|||||
Sbjct: 104742 gttgaaacgc 104733

>AC007344 ACCESSION:AC007344 NID: gi 5851724 gb AC007344.3 AC007344 Homo
sapiens chromosome 16 clone RPCI-11_466G2, complete
sequence
Length = 180827

Score = 589 bits (297), Expect = e-165
Identities = 309/310 (99%), Gaps = 1/310 (0%)
Strand = Plus / Plus

Query: 1 ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 60
|||||
Sbjct: 176532 ggaagctttcacaccacattttgtttcctgacaagagaaggagaaatcgttggcctctgc 176591

Query: 61 gtgacatggagggtccccccacctgcaagcttttggtttgctggatcttggacagtacc 120
|||||
Sbjct: 176592 gtgacatggagggtccccccacctgcaagcttttggtttgctggatcttggacagtacc 176651

Query: 121 ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 180
|||||
Sbjct: 176652 ctggcgaaaagcattcggcaagattatccggctagcacagccttcaaggaataaatatct 176711

Query: 181 aacaccttggtccc-tttgcggttcaaaagccactgtcactgggggtacataggcagtttt 239
|||||
Sbjct: 176712 aacaccttggtcccttttgcggttcaaaagccactgtcactgggggtacataggcagtttt 176771

Query: 240 aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 299
|||||
Sbjct: 176772 aaaaaaggctacaattcatatgcaaactagaggaggatttccatgatttcataataaaat 176831

Query: 300 gttgaaacgc 309
|||||
Sbjct: 176832 gttgaaacgc 176841

Query= SEQ ID NO:11 (PE029)
(143 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8 Hom...	<u>266</u>	1e-68
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>AC019129 ACCESSION:AC019129 NID: gi 16077059 gb AC019129.8 Homo
sapiens BAC clone RP11-559M23 from 2, complete sequence
Length = 172611

Score = 266 bits (134), Expect = 1e-68
Identities = 140/143 (97%)
Strand = Plus / Minus

Query: 1	gtggccatgtacttggcttaaagttaaggattctactactgtngaaganggagagaacgg	60
Sbjct: 94486	gtggccatgtacttggcttaaagttaaggattctactactgtagaagaaggagagaacgg	94427

Query: 61	nttctagaggacaactggcagtcctccttgtagctgagacttttttgtgtataaaaattaa	120
Sbjct: 94426	attctagaggacaactggcagtcctccttgtagctgagacttttttgtgtataaaaattaa	94367

Query: 121	taaaattgggtttattaatttggt	143
Sbjct: 94366	taaaattgggtttattaatttggt	94344

Query= SEQ ID NO:12 (PE029)
(210 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC016601.7.1.145264	<u>281</u>	8e-74
AC034246.4.1.155025	<u>281</u>	8e-74

>AC016601.7.1.145264
Length = 145264

Score = 281 bits (142), Expect = 8e-74
Identities = 146/147 (99%), Gaps = 1/147 (0%)
Strand = Plus / Minus

Query: 64 agagatgggggtttcgccatggtgccaggtggtctcaagctcctgaactcaagtgatc 123
||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36474 agagat-ggggtttcgccatggtgccaggtggtctcaagctcctgaactcaagtgatc 36416

Query: 124 ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 183
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 36415 ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 36356

Query: 184 aaatatagattttaatcttcagcttgc 210
|||||||||||||||||||||||||||
Sbjct: 36355 aaatatagattttaatcttcagcttgc 36329

Score = 129 bits (65), Expect = 7e-28
Identities = 65/65 (100%)
Strand = Plus / Minus

Query: 1 atctatgcagattagctctctgcccttcctttaataactggactcttgagcatctgatt 60
|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 43711 atctatgcagattagctctctgcccttcctttaataactggactcttgagcatctgatt 43652

Query: 61 gacag 65
|||||
Sbjct: 43651 gacag 43647

>AC034246.4.1.155025
Length = 155025

Score = 281 bits (142), Expect = 8e-74
Identities = 146/147 (99%), Gaps = 1/147 (0%)
Strand = Plus / Plus

Query: 64 agagatgggggtttcgccatggtgccaggetggtctcaagctcctgaactcaagtgatc 123
||||| |||||||
Sbjct: 16092 agagat-ggggtttcgccatggtgccaggetggtctcaagctcctgaactcaagtgatc 16150

Query: 124 ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 183
|||||
Sbjct: 16151 ttcccacctaagcctcccaaagtgctgggattacaggcatgagccacgactcccagcctg 16210

Query: 184 aaatatagattttaatcttcagcttgc 210
|||||
Sbjct: 16211 aaatatagattttaatcttcagcttgc 16237

Score = 129 bits (65), Expect = 7e-28
Identities = 65/65 (100%)
Strand = Plus / Plus

Query: 1 atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 60
|||||
Sbjct: 8857 atctatgcagattagctctctgcccttcctttaataactggactcttggagcatctgatt 8916

Query: 61 gacag 65
|||||
Sbjct: 8917 gacag 8921

Query= SEQ ID NO:13 (PE029)
(453 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 H...	<u>735</u>	0.0
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>AL391500 ACCESSION:AL391500 NID: gi 12227422 emb AL391500.13 Human DNA
sequence from clone RP11-707M13 on chromosome 6, complete
sequence
Length = 171220

Score = 735 bits (371), Expect = 0.0
Identities = 371/371 (100%)
Strand = Plus / Minus

Query: 1	gtatacatccagatggccggaagcaactgaagatccacaaaagaagtgaaaatagccgta	60
Sbjct: 76957	gtatacatccagatggccggaagcaactgaagatccacaaaagaagtgaaaatagccgta	76898

Query: 61	actgatgacattccaccattgtgatttgtttctgccccaccgtaactgatcaatgtactt	120
Sbjct: 76897	actgatgacattccaccattgtgatttgtttctgccccaccgtaactgatcaatgtactt	76838

Query: 121	tgtaatctccccacccttaagaaggttctttgtaatctccccacccttaagaatgttc	180
Sbjct: 76837	tgtaatctccccacccttaagaaggttctttgtaatctccccacccttaagaatgttc	76778

Query: 181	tttgtaattctccccacccttgagaatgtactttgtgagatctaccccctgccacaaaa	240
Sbjct: 76777	tttgtaattctccccacccttgagaatgtactttgtgagatctaccccctgccacaaaa	76718

Query: 241	cattggtcctgactccaccgcctatcccaaacctataagaactaatgataatcccacca	300
Sbjct: 76717	cattggtcctgactccaccgcctatcccaaacctataagaactaatgataatcccacca	76658

Query: 301	ccctttgctgactctcttttcggactcagcccgctgcacccaggtgaaataaacagcct	360
Sbjct: 76657	ccctttgctgactctcttttcggactcagcccgctgcacccaggtgaaataaacagcct	76598

Query: 361	tgttgctcaca	371
Sbjct: 76597	tgttgctcaca	76587

Query= SEQ ID NO:14 (PE029)
(344 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AL354814.19.1.70126	<u>281</u>	1e-73
AL391683.8.1.168373	<u>238</u>	2e-60
AL160397.17.1.204056	<u>163</u>	2e-38

>AL354814.19.1.70126
Length = 70126

Score = 281 bits (142), Expect = 1e-73
Identities = 145/146 (99%)
Strand = Plus / Plus

Query: 199 caggaagaaaaatggaactaaaaagggaaaacaatagcaacaaagatcaaaataaataac 258
|||||
Sbjct: 25129 caggaagaaaaatggaactaaaaagggaaaacaatagcaacaaagatcaaaataaataac 25188

Query: 259 aaggaagcggagagaagaaagaacatggtgaagagagtgaaaagcattgtcatttgggggt 318
|||||
Sbjct: 25189 aaggaagcggagagaagaaagaacatggtgaagagagtgaaacgcattgtcatttgggggt 25248

Query: 319 gaattgcagaaagaaataaattattg 344
|||||
Sbjct: 25249 gaattgcagaaagaaataaattattg 25274

>AL391683.8.1.168373
Length = 168373

Score = 238 bits (120), Expect = 2e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 83 aatttcgctcttggtgcccaggctggagtgcaatgacgagatcttggctcactgcaacct 142
|||||
Sbjct: 140792 aatttcgctcttggtgcccaggctggagtgcaatgacgagatcttggctcactgcaacct 140851

Query: 143 ccacctcccaggtttaagtgattctcctgcctcagcctcccaagtagctgggattacagg 202
|||||
Sbjct: 140852 ccacctcccaggtttaagtgattctcctgcctcagcctcccaagtagctgggattacagg 140911

>AL160397.17.1.204056
Length = 204056

Score = 163 bits (82), Expect = 2e-38
Identities = 82/82 (100%)
Strand = Plus / Plus

Query: 1 tgcctccagaaagaacgcagccctactgacaccttggttttggcctggtgagaccaactt 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1502 tgcctccagaaagaacgcagccctactgacaccttggttttggcctggtgagaccaactt 1561

Query: 61 tggacttttcacttccaaaact 82
||||||||||||||||||||
Sbjct: 1562 tggacttttcacttccaaaact 1583

Query= SEQ ID NO:15 (PE029)
(473 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6 Hom...	<u>414</u>	e-113
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>AC084117 ACCESSION:AC084117 NID: gi 22165345 gb AC084117.6 Homo
sapiens chromosome 11, clone RP11-107C21, complete
sequence
Length = 166973

Score = 414 bits (209), Expect = e-113
Identities = 215/217 (99%)
Strand = Plus / Minus

Query: 192 caggtctacatttctctttgccatactgctctgggctctgggggttgacctgaatggacc 251
|||||
Sbjct: 84399 caggtctacatttctctttgccatactgctctgggctctgggggttgacctgaatggacc 84340

Query: 252 acacagccatgggtgtctcctgtcctccaccttcactgggtgaagactgggagtgaggaaga 311
|||||
Sbjct: 84339 acacagccatgggtgtctcctgtcctccaccttcactgggtgaagactgggagtgaggaaga 84280

Query: 312 agagtgagattgcaccctctctgcaggaccatgggcagaccctgccccttacctcttctc 371
|||||
Sbjct: 84279 agagtgagattgcaccctctctgcaggaccatgggcagaccctgccccttacctcttctc 84220

Query: 372 aggggtctctcttctctcctattaacttctttccatt 408
|||||
Sbjct: 84219 aggggtctctcttctctcctgttaacttctttccatt 84183

Query= SEQ ID NO:16 (PE029)
(403 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AP003031.3.1.95585	<u>456</u>	e-126
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>AP003031.3.1.95585
Length = 95585

Score = 456 bits (230), Expect = e-126
Identities = 240/243 (98%), Gaps = 1/243 (0%)
Strand = Plus / Minus

```
Query: 161   gagccaagaagtcctcaaagcccttcctaaaggatggaggaacacatgaatatatacatc 220
           |||
Sbjct: 27019 gagccaagaagtcctcaaagcccttcctaaaggatggaggaacacatgaatatatacatc 26960
```

```
Query: 221   aaatcctccttccacagagactcactgaagggaatgaagaagggaagaaagtcctcctaatt 280
           |||
Sbjct: 26959 aaatcctccttccacagagactcactgaagggaatgaagaagggaagaaagtcctcctaatt 26900
```

```
Query: 281   attaagatgcgttccttgggactcggagaattaggaaggaaaccccccaagtcttgaatac 340
           |||
Sbjct: 26899 attaagatgcgttccttgggactcggagaattaggaaggaaaccccccaagtcttgaatac 26840
```

```
Query: 341   atttctctaaagaggccgaataacttaataatcaggggagattaaagcaaagggagac-c 399
           |||
Sbjct: 26839 atttctctaaagaggccgaataacttaataatcaggggagattaaagcaaagggtagacac 26780
```

```
Query: 400   cct 402
           |||
Sbjct: 26779 cct 26777
```

Score = 311 bits (157), Expect = 2e-82
Identities = 160/161 (99%)
Strand = Plus / Minus

```
Query: 1     gagtctactgacagaagccaaagggttgctgctagtttcagcttcctggtgttcctcatta 60
           |||
Sbjct: 37882 gagtctactgacaaaagccaaagggttgctgctagtttcagcttcctggtgttcctcatta 37823
```

```
Query: 61    ttttcaaaaatgtctgactgcacatcttttggacattataaaaaccacagtaggaaaaaacg 120
           |||
Sbjct: 37822 ttttcaaaaatgtctgactgcacatcttttggacattataaaaaccacagtaggaaaaaacg 37763
```

```
Query: 121   ccagctatttcaatggaccaacaaagtgagactccaaagtg 161
            ||||||||||||||||||||||||||||||||||||
Sbjct: 37762 ccagctatttcaatggaccaacaaagtgagactccaaagtg 37722
```

Query= SEQ ID NO:17 (PE029)
(445 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AL158141.14.1.184181	<u>535</u>	e-150
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>AL158141.14.1.184181
Length = 184181

Score = 535 bits (270), Expect = e-150
Identities = 312/329 (94%), Gaps = 2/329 (0%)
Strand = Plus / Plus

Query: 118 aggggtcttgctctgtcgcccaggctagagtgcagtgggcgcaatcttggtcatggcaacc 177
|||||
Sbjct: 9434 aggggtcttgctctgtcgcccaggctagagtgcagtgggcgcaatcttggtcatggcaacc 9493

Query: 178 tccacctcccggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 237
|||||
Sbjct: 9494 tccacctcccggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 9553

Query: 238 gtgcctaccaccaggcccagctaaatTTTTTgtatTTTtagtacagacggggTTTcgcc 297
|||||
Sbjct: 9554 gtgcctaccaccaggcccagctaaatTTTTTgtatTTTtagtacagacggggTTTcgcc 9613

Query: 298 accttggccaggctggtcttgaactcctgaccttgatctacccacctnagnntcccaa 357
|||||
Sbjct: 9614 accttggccaggctggtcttgaactcctgaccttgatctacccacctcagctcccaa 9673

Query: 358 ngggctgggnattacaggggggagagaccggaccacaccttactgngtttctgantgn 417
| |||||
Sbjct: 9674 agtgctgggattacagggtgtgagagaccgcaccacaccttactgagtttctgattgc 9733

Query: 418 nntttcctttcct-ttccttttcccttaa 445
|||||
Sbjct: 9734 tctttcctt-cctcttccttctcccttaa 9761

Score = 238 bits (120), Expect = 2e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1 agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatagacctc 60
|||||
Sbjct: 8124 agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatagacctc 8183

Query: 61 ctgcctcagcctcccaaagtgtgcgattaaaggcacaagccactgtgcccaaccaaagg 120
|||||
Sbjct: 8184 ctgcctcagcctcccaaagtgtgcgattaaaggcacaagccactgtgcccaaccaaagg 8243

Query= SEQ ID NO:18 (PE029)
(486 letters)

Sequences producing significant alignments:	Score (bits)	E Value
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AL158141.14.1.184181	<u>599</u>	e-169
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>AL158141.14.1.184181
Length = 184181

Score = 599 bits (302), Expect = e-169
Identities = 347/362 (95%), Gaps = 3/362 (0%)
Strand = Plus / Plus

Query: 118 aggggtcttgctctgtcgcccaggctagagtgcagtgggcgcaatcttgggtcatggcaacc 177
|||||
Sbjct: 9434 aggggtcttgctctgtcgcccaggctagagtgcagtgggcgcaatcttgggtcatggcaacc 9493

Query: 178 tccacctcccggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 237
|||||
Sbjct: 9494 tccacctcccggttcaagcgattctcctgccacagcctcccgagtagctgggattacag 9553

Query: 238 gtgcctaccaccaggcccagct-aatTTTTTTgtatTTTTtagtacagacggggTTTcgcc 296
|||||
Sbjct: 9554 gtgcctaccaccaggcccagctaaatTTTTTTgtatTTTTtagtacagacggggTTTcgcc 9613

Query: 297 accttggccaggctggtcttgaactcctgaccttgatctaccacctcagtctcccaa 356
|||||
Sbjct: 9614 accttggccaggctggtcttgaactcctgaccttgatctaccacctcagtctcccaa 9673

Query: 357 agtgctgggattacagggtgtgagagaccgcacccaggcaccttactgaggttctgaatgn 416
|||||
Sbjct: 9674 agtgctgggattacagggtgtgagagaccgcacccaggcaccttactgagtttctgattgc 9733

Query: 417 tcttttcnttctttttcctttttcccttaaattggcccaaagtttnatccttggttttt 476
|||||
Sbjct: 9734 tctttcc-ttcctcttccttct-cccttaacttgcccaaagttttatccttgacttttt 9791

Query: 477 tt 478
||
Sbjct: 9792 tt 9793

Score = 238 bits (120), Expect = 3e-60
Identities = 120/120 (100%)
Strand = Plus / Plus

Query: 1 agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatagacctc 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8124 agacgggggtctcactacgttgcccaggctgatcttgaactcctgcctcaaatagacctc 8183

Query: 61 ctgcctcagcctcccaaagtgtgcgattaaaggcacaagccactgtgcccaccaaagg 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 8184 ctgcctcagcctcccaaagtgtgcgattaaaggcacaagccactgtgcccaccaaagg 8243